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GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1371.68 Seconds
(without alignment)
12007.805 Million cell updates/sec

Title: US-09-807-933B-8
Perfect score: 1017
Sequence: 1 atgaagtcaccgcgtgctat.....caggttcgaaagaagtaa 1017

Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_eacba:*
2: em_eacbm:*
3: em_eactin:*
4: em_eactm:*
5: em_eactov:*
6: em_eactpl:*
7: em_eactro:*
8: em_hlc:*
9: gb_eactl:*
10: gb_eact2:*
11: gb_hlc:*
12: gb_eact3:*
13: gb_eact4:*
14: gb_eact5:*
15: em_eactfun:*
16: em_eactom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	17.0	691	10	BE585661 EST#6PSP6
2	122.2	12.0	450	13	BT200729
3	111	10.9	444	13	BT190695
4	104.4	10.3	426	13	BT187295
5	81.2	8.0	215	13	BT190568
6	73.6	7.2	989	17	CNS02HAA4

7	72	7.1	494	17	FR0048073	AL444858 Fugu rubr
8	70.8	7.0	350	17	BH879665	BH879665 hc47n12.9
9	70.6	6.9	450	17	FR0025683	AL018519 F. rubripes
10	70.6	6.9	501	17	PR0048173	AL44958 Fugu rubr
11	70	6.9	914	17	AZ205202	AZ205202 SP_0100_A
12	69.6	6.8	933	17	AZ204694	AZ204694 SP_0100_A
13	67.8	6.7	788	17	AZ183942	AZ183942 SP_1002_A
14	67.2	6.6	627	17	BH179321	BH179321 014_P_01-
15	67.2	6.6	627	17	CNS07LFL	AL616275 T7 end of
16	66	6.5	735	17	CNS04NSM	AL299119 Tetradon
17	65.8	6.5	335	10	AW275677	AW275677 xp08e07.x
18	65.8	6.5	619	17	FR0047601	AL444386 Fugu rubr
19	65.6	6.5	570	17	AZ149014	AZ149014 SP_0020_B
20	65.2	6.4	530	17	AZ166409	AZ166409 SP_0088_A
21	64.8	6.4	392	17	FR0048008	AL444793 Fugu rubr
22	64.2	6.3	331	17	BH881398	BH881398 hv25c11.b
23	64.2	6.3	773	17	CNS01VVG	AL169549 Tetradon
24	64	6.3	500	17	B67199	B67199 CpG0015B Cp
25	63.8	6.3	354	17	AQ935615	AQ935615 CpG2561B
26	63.4	6.2	250	17	BH878991	BH878991 hb85e08.b
27	63.2	6.2	824	17	AZ185454	AZ185454 SP_1005_A
28	62.6	6.2	522	13	BT783235	E1783235 K478909.Y
29	62.6	6.2	621	17	AZ164800	AZ164800 SP_0076_B
30	62.2	6.1	358	17	BH777606	BH777606 f2mb013f0
31	62.2	6.1	580	17	BH763893	BH763893 BMBAC314F
32	62	6.1	177	17	BH881173	BH881173 hv23q03.b
33	62	6.1	204	17	BH882682	BH882682 hv38h10.g
34	62	6.1	230	17	BH869848	BH869848 hm54h10.g
35	62	6.1	510	13	BT374789	BT374789 BT374789
36	62	6.1	619	17	FR0006944	Z90754 F. rubripes
37	62	6.1	810	17	AZ199472	AZ199472 SP_1039_B
38	61.8	6.1	218	17	BH875125	BH875125 hbG3h02.g
39	61.2	6.0	795	17	AZ186967	AZ186967 SP_1008_A
40	60.6	6.0	454	17	AZ178507	AZ178507 SP_0161_B
41	60.2	5.9	976	17	CNS01FBX	AL141646 Anopheles
42	60	5.9	558	17	AZ146816	AZ146816 SP_0047_B
43	59.8	5.9	539	9	AT002510	AT002510 AT002510
44	59.6	5.9	485	13	BT370491	BT370491 BT370491
45	59.4	5.8	196	17	PR0047508	AL444293 Fugu rubr

ALIGNMENTS

RESULT 1
BE585661
LOCUS
DEFINITION
CDNA library Trilicium aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.

ACCESSION
BE585661
VERSION
BE585661.1 GI:9838604

KEYWORDS
SOURCE
ORGANISM

EST.
bread wheat.
Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
1 (bases 1 to 691)
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.

REFERENCE
AUTHORS
TITLE
The structure and function of the expressed portion of the wheat
genomes - Kansas State University, Fusarium graminearum infected
spike CDNA library

JOURNAL
COMMENT
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SP6.

FEATURES

Source

Location/Qualifiers
1..691
/organism="Triticum aestivum"
/cultivar="Suma13"
/db xref="taxon:4565"
/clone="EST#6PSP6.D02.d2.014"
/clone.lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/cissue.type="Spike"
/dev stage="Adult plant"
/lab host="E. coli JM109"
/note="vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
plants were grown in the greenhouse. Spikes were infected
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

ORIGIN

Query Match 17.0%; Score 173; DB 10; Length 691;
Best Local Similarity 63.8%; Pred. No. 1,1e-38;
Matches 279; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

OY 400 TCTGGCAAGTGTTCACCACTGCTTATTGGATTGTTAAAGCTTCTTGACAGCTGCT 459
DB 168 TCTGGCAAGTGTTCACCACTGCTTATTGGATTGTTAAAGCTTCTTGACAGCTGCT 227
OY 460 GGAAGAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
DB 228 GGCAGAGCCCAAGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
OY 520 GATGCAAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
DB 288 AACCTGAAGCCGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 347
OY 577 CAACCTGGGCTGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 636
DB 348 TCCCTTGGGCTGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 407
OY 637 TCCAGCAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
DB 408 GGCAGTGAAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 467
OY 697 TCTGGAAGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 756
DB 468 AAGGGAAGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 527
OY 757 TTGGATTGGCAATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
DB 528 TTGGACCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
OY 817 GGCCTCTCCCAATGATG 833
DB 588 GGCAGGCTCTCGGTGG 604

RESULT 2

BI200729 450 bp mRNA linear EST 10-JUN-2001
LOCUS o1f05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone o1f05fs 5', mRNA
sequence.

ACCESSION BI200729
VERSION BI200729.1 GI:14666701
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
AUTHORS Ren, Q., Isg, A., Fedlow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
TITLE 'M. and Roe, B.
JOURNAL Analysis of a Fusarium sporotrichioides EST database
COMMENT Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
633 5e-66 g11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KRECURSOR (EN
Seq primer: T3
High quality sequence stop: 440.

FEATURES

Source

Location/Qualifiers
1..450
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db xref="taxon:5514"
/clone="o1f05fs"
/clone.lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

ORIGIN

Query Match 12.0%; Score 122.2; DB 13; Length 450;
Best Local Similarity 63.6%; Pred. No. 4e-24;
Matches 203; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

OY 400 TCTGGCAAGTGTTCACCACTGCTTATTGGATTGTTAAAGCTTCTTGACAGCTGCT 459
DB 132 TCTGGCAAGTGTTCACCACTGCTTATTGGATTGTTAAAGCTTCTTGACAGCTGCT 191
OY 460 GGAAGAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
DB 192 GGCAGAGCCCAAGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
OY 520 GATGCAAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
DB 252 AACCTGAAGCCGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
OY 577 CAACCTGGGCTGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 636
DB 312 TCCCGTGGGCTGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 371
OY 637 TCCAGCAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
DB 372 GGTATGAGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 431
OY 697 TCTGGAAGAAGTGTGT 715
DB 432 AAGGCAAGAAGTGTGT 450

RESULT 3

BI190695 444 bp mRNA linear EST 10-JUN-2001
LOCUS i3g10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
sequence.

ACCESSION BI190695
VERSION BI190695.1 GI:14664374
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE TITLE
AUTHORS JOURNAL
COMMENT

Hypocretales; mitosporic Hypocretales; Fusarium.
1 (bases 1 to 444)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broeou@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01
576 38-59 g|1170140|bp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3.
Location/Qualifiers
1. 444
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="13910f8"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 85 a 127 c 92 g 140 t
ORIGIN

Query Match 10.9%; Score 111; DB 13; Length 444;
Best Local Similarity 64.1%; Pred. No. 6.8e-21;
Matches 184; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

400 TCTGGAGTGGTTCACAACTCGTATAGGATTGTAAAGCTTCTTGACGCTGCT 459
158 TCTGGAAGTGGCCACTCTACTCGATCTGGAGCTGCTCAACCTTCTTGCTTGAGC 217
460 GGAAGAGCTTCTGCTACTGCTCTGTTGACACTGCTGCTCAATGATCTCTTATTA 519
218 GGAAGAGTAAAGTCAGAGCCCTGCTGCTGATGACAAAGATTAACCTATATCT 277
400 GATGCCAATGCTCAAGTGTGTTGA---CGGTGTAATGCTTCAATGTAACCAAC 576
278 AACTGAAAGCTGTCAACGGTTGAGGGGTGCTGCTTATGCTTGACCAACTAC 337
400 CAACCTTGGGCTGTCATATGATGAGCTGCTTACGGTTGCGAGCTCTTATGCTGGC 636
338 TCCCGTGGGCTGTCAACGACGACCTTGCCTTACGGTTGCGCTACCAAGCTTGCT 397
400 TCCAACGAGCTGATGATGTTGCTGCTTATGTAATGACCTTAC 683
398 GGTAGTAGGCGCAGCTGCTGCTGCTATGCTCACTTAC 444

RESULT 4
LOCUS B1187295 426 bp mRNA linear EST 10-JUL-2001
DEFINITION B1187295.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone ah11f5 5', mRNA
SEQUENCE
B1187295
B1187295.1 GI:14660974
EST.
SOURCE
ORGANISM
Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocretales; mitosporic Hypocretales; Fusarium.
REFERENCE
1 (bases 1 to 426)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.

TITLE
JOURNAL
COMMENT

Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other ESTs: ah11f5.f1
Contact: Bruce A. Roe, University of Oklahoma, broeou@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01
565 5e-58 g|1170140|bp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 338.
Location/Qualifiers
1. 426
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="ah11f5"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 82 a 119 c 91 g 134 t
ORIGIN

Query Match 10.3%; Score 104.4; DB 13; Length 426;
Best Local Similarity 63.9%; Pred. No. 5.3e-19;
Matches 175; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

400 TCTGGAGTGGTTCACAACTCGTATAGGATTGTAAAGCTTCTTGACGCTGCT 459
148 TCTGGAAGTGGCCACTCTACTCGATCTGGAGCTGCTCAACCTTCTTGCTTGAGC 207
460 GGAAGAGCTTCTGCTACTGCTCTGTTGACACTGCTGCTCAATGATCTCTTATTA 519
208 GGAAGAGTAAAGTCAGAGCCCTGCTGCTGATGACAAAGATTAACCTATATCT 267
400 GATGCCAATGCTCAAGTGTGTTGA---CGGTGTAATGCTTCAATGTAACCAAC 576
268 AACTGAAAGCTGTCAACGGTTGAGGGGTGCTGCTTATGCTTGACCAACTAC 327
400 CAACCTTGGGCTGTCATATGATGAGCTGCTTACGGTTGCGAGCTCTTATGCTGGC 636
328 TCCCGTGGGCTGTCAACGACGACCTTGCCTTACGGTTGCGCTACCAAGCTTGCT 387
400 TCCAACGAGCTGATGATGTTGCTGCTTATGTAATGACCTTAC 670
388 GGTAGTAGGCGCAGCTGCTGCTGCTATGCTCACTTAC 421

RESULT 5
LOCUS B1190568 215 bp mRNA linear EST 10-JUL-2001
DEFINITION B1190568.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 12ah1f5 5', mRNA
SEQUENCE
B1190568
B1190568.1 GI:14664247
EST.
SOURCE
ORGANISM
Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocretales; mitosporic Hypocretales; Fusarium.
REFERENCE
1 (bases 1 to 215)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.

TITLE
JOURNAL
Unpublished (2001)

JOURNAL

Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:

COMMENT

biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS

FEATURES

source

One pass dye-terminator sequencing of BAC (pBelobACII) cloned genomic sequence
The BACs can be obtained from <http://www.inkycie.com>.
Location/Qualifiers

BASE COUNT 128 a 163 c 45 g 158 t
ORIGIN

Query Match 7.1%; Score 72; DB 17; Length 494;
Best Local Similarity 50.3%; Pred. No. 1.3e-09;
Matches 177; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

207 TGTGTGTAACGCTAGACAGACCAAGACATCTACCAAGACATCTACACCGCCAA 266
119 TGTCTTACTACTGCTACTACTACTAGACAGCTGCTACTACTACTGCTACTACTACTAC 178
267 GGTCTACTGCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 326
179 TACTACTACTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 238
327 GACTAGACACTACTGCGCTGCTCTTCTTCCACCGCTTCTTCTGCTGCTTCAAGTCAT 386
239 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 298
387 CTCTGGCGGTAAATCTGGCAGTGTTCACCACTGTTATTTGAGATTGTTGTAAGCTTC 446
299 TACTACTGCTACTACTACTACTACTACTACTACTACTACTGCTGCTACTGCTGCTACTAC 358
447 TTGACAGCTGCTGGAAGGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
359 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 418
507 TATCTCTTATTAGATGCGCAATGCTCAAGTGTGTTAGCGTGGTATGCT 558
419 TACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTGCT 470

RESULT 8
BH879665 350 bp DNA linear GSS 05-AUG-2002
LOCUS h47h12.g1 WGS-2may9f (JM107 adapted methyl filtered) Zea mays

ACCESSION BH879665
VERSION BH879665.1 GI:22115562
KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascentino, L., Zuber, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874

COMMENT

Email: mccombie@cshl.org
Plate: h47 row: h column: 12
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 350.
Location/Qualifiers

FEATURES

source

One pass dye-terminator sequencing of cosmid cloned genomic
DESCR: 1. .350
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="h47h12"
/lab_host="JM107 or DH5a"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 112 a 110 c 13 g 115 t
ORIGIN

Query Match 7.0%; Score 70.8; DB 17; Length 350;
Best Local Similarity 53.2%; Pred. No. 2.4e-09;
Matches 150; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

199 AGTAAATGCTGTGTAACGCTAGACAGACCAAGACATCTACCAAGACATCTACTACC 258
49 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 108
259 ACCGCCAAGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCT 318
109 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 168
319 ACTACCAAGCTAGCACTACTGCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 378
169 AGCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
379 AAGGTACTCTGCGGTAAATCTGGCAGTGTTCACCACTGTTATTTGAGATTGTTGT 438
229 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 288
439 AAGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
289 ACTACTACTAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 330

RESULT 9
FR0025683 450 bp DNA linear GSS 10-DEC-1997
LOCUS F.rubripes GSS sequence, clone 154E17a12, genomic survey sequence.

ACCESSION AL018519
VERSION AL018519.1 GI:2684887
KEYWORDS GSS: genome survey sequence.

SOURCE Takifugu rubripes.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

REFERENCE

AUTHORS

Elgar, G., Clark, M., Smith, S., Week, S., Warner, S., Umranta, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk

COMMENT

Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

FEATURES

source

Location/Qualifiers
1..450
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 154E17"

BASE COUNT 96 a 140 c 64 g 144 t 6 others

Query Match
Best Local Similarity 50.4%; Score 70.6; DB 17; Length 450;
Matches 172; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

218 CTAGCAGCACCAGAGACATCTACCAAGACATCTACCAAGCAGGCTACTGCTA 277
78 CTACTACTACTACTGCTACTGCTACTACTGCTACTACTACTACTACTACTACTA 137
278 CTGTCAACCAAGACAGTAACTACCAAGACATCTACCAAGCAGGCTACTGCTA 337
138 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 197
338 CTGCGGCTCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 397
198 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 257
398 AATCTGGCAGTGGTTCACAACTCGTTATTTGGATTGTGTAAGCTTCTGCAAGTGC 457
258 CTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 317
458 CTGGAAAGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 517
318 CTATTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 377
518 TAGATGCCATGCTCAAGTGGTGTGAACGCTGTGTAATGTT 558
378 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 418

RESULT 10
FR0048173 501 bp DNA linear GSS 05-JAN-2001
LOCUS Fugu rubripes GSS sequence, clone 264E22CA9, genomic survey
DEFINITION

ACCESSION
AL444958
VERSION
GI:12053458
KEYWORDS
GSS; genome survey sequence.
SOURCE
Takifugu rubripes
ORGANISM
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.

REFERENCE
1 (bases 1 to 501)
Clark, M.S.
Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB, UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of BAC (pBelobAC11) cloned
genomic sequence
The BACs can be obtained from <http://www.incyte.com>.

FEATURES
source
1..501
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="264E22CA9"
/clone_lib="BAC 264E22"

BASE COUNT 132 a 161 c 35 g 173 t

ORIGIN

Query Match
Best Local Similarity 50.1%; Score 70.6; DB 17; Length 501;
Matches 175; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

207 TGTGTGTAACGCTAGACAGCACCAGAGACATCTACCAAGACATCTACTACAGCCCA 266
140 TGCTTCTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 199
267 GGCTACTGCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 326
200 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 259
327 GACTGACTACTGCGGCTGCTCTCTACTCTCCACCTCTCTCTGCTGCTCAAGGCTAT 386
260 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTGC 319
387 CTGCGGCTTAATCTGGCAGTGGTTCACAACTCGTTATTTGGATTGTGTAAGCTTC 446
447 TTGACAGCTGGCTGGAAAGCTTCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
380 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTG 439
507 TATCTCTTATTAAGATGCGCAATGCTCAAGTGGTGTGTAACGCTGTAAT 555
440 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAG 488

RESULT 11
A2205202 914 bp DNA linear GSS 31-AUG-2000
LOCUS SP 0100_A2 G12 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus
DEFINITION
A2205202
A2205202.1 GI:8400122
GSS.
Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoda;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 914)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Foustka, A.V., Livingston, B.T., Wray,
G.A., Eitelsohn, C.A., Lehnach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-1047
Email: acameron@caltech.edu
Plate: 100 row: M column: 24
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 914.

FEATURES
source
1..914
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=100 COL=24 ROW=M"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACs; 6; BAC clones in E-Coli

BASE COUNT 210 a 208 c 107 g 387 t 2 others
 DH10B[®]
 ORIGIN

Query Match 6.9%; Score 70; DB 17; Length 914;
 Best Local Similarity 48.7%; Pred. No. 7.5e-09;
 Matches 190; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

199 AGTAACATGCTGGTAACGCTAGACGACCAAGACATCTACCAAGATCTACTACC 258
 169 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
 259 ACCGCCAAGGCTACTGCTACTGTCACCAAGACAGTAACCAAGACATCCAGACA 318
 229 ACCACCACTACTACTACTGCACTACTACTACTACTACTACTACTACTACTACT 288
 319 ACTACCAAGACTACTACTGCGCTGCTCTTCACTTCCACTCTTCTTCTGCTGTTAC 378
 289 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 348
 379 AAGCTACTCTGCGGTAATCTGGAGTGTCCCACTCGTTATGGGATTTGT 438
 349 ACTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 408
 439 AAGCTTCTGCACTGCGCTGGAAGCTTCTGCTACTGCTCTGTTGACACCTGTGCC 498
 409 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 468
 499 TCCAAATGATCTCTTTATTAGATGCCAATGCTCAAGTGTGTAAAGTGTATGT 558
 469 ACTAATGTGATGTTAATTTATTTATTTCTTTCAATATGACCTGCGTGTCTTGG 528
 559 TTCAATGTGTACACACCAACCTTGGGCT 588
 529 TTGTATATATATATATATATATATATATATATATATATATATATATATATAT 558

RESULT 12
 AZ204694 933 bp DNA linear GSS 31-AUG-2000
 LOCUS
 DEFINITION SP_0100_A1.G12.SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=23 Row=M, DNA sequence.

ACCESSION AZ204694 GI:8399614
 VERSION
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidae; Euechinoidae; Echinacea; Echinoidae;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 933)
 Cameron,R.A., Mahatras,G., Raet,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL MEDLINE
 COMMENT Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 20402566
 Contact: Cameron, RA, Davidson, EH, Hood, L
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 100 row: M column: 23
 Seg primer: SP6
 Class: BAC ends
 High quality sequence stop: 933.
 Location/Qualifiers
 1..933

FEATURES
 source

/organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="plate=100 Col=23 Row=M"
 /clone_1b="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"
 BASE COUNT 226 a 235 c 156 g 316 t
 ORIGIN

Query Match 6.8%; Score 69.6; DB 17; Length 933;
 Best Local Similarity 48.9%; Pred. No. 9.9e-09;
 Matches 186; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

189 CGATCCCAAGTAACATGCTGTAACGCTAGACGACCAAGACATCTACCAAGAC 248
 110 GCAATACACCGTCAATCTACTACTACTACTACTACTACTACTACTACTACTACT 169
 249 ATCTACTACACCGCCAGGCTACTGCTGTCACCAAGACAGTAACCAAGAAC 308
 170 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 229
 309 TACCAAGACACTACCAAGCTAGACACTACTGCGCTTCTTCACTTCCACTCTTCTC 368
 230 CACCACTACTACTACTTCCACTATTACTACTACTACTACTACTACTACTACTACT 289
 369 TCGTGTAGAGTCACTCTGCGGTAATCTGGAGTGTTCACCACTGTTATTTG 428
 290 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 349
 429 GATTTGTTGAAGCTTCTGCACTGCGCTGGAAGCTTCTGCTACTGCTCTGTTGA 488
 350 TGCATATTTACTACTACTCTTCTACTACTACTACTACTACTACTACTACTACTACT 409
 489 CACCTGTGCTCCAAATGATCTTTATTAGATGCCAATGCTCAAGTGTGTAAAG 548
 410 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 469
 549 TCGTAATGTTTCAATGTGA 568
 470 TAATGATGATTAATTTATA 489

RESULT 13
 AZ183942 788 bp DNA linear GSS 30-AUG-2000
 LOCUS
 DEFINITION SP_1002_A1.H11.SP6 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1002 Col=21 Row=O, DNA sequence.

ACCESSION AZ183942 GI:8356317
 VERSION
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidae; Euechinoidae; Echinacea; Echinoidae;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 788)
 Cameron,R.A., Mahatras,G., Raet,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL MEDLINE
 COMMENT Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 20402566
 Contact: Cameron, RA, Davidson, EH, Hood, L
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu

to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformation. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

FEATURES

source

Location/Qualifiers

1. 627

/organism="Schistosoma mansoni"

/strain="Puerto-Rican"

/db_xref="taxon:6183"

/clone="014CH01"

/clone_lib="SMBAC1"

/note="end : T7"

BASE COUNT 169 a 79 c 196 g 167 t 16 others

ORIGIN

Query Match

6.6%; Score 67.2; DB 17; Length 627;

Best Local Similarity 52.3%; Pred. No. 3.8e-08;

Matches 135; Conservative 5; Mismatches 118; Indels 0; Gaps 0;

```
OY 226 ACCAAGAAGCATCTACCAAGACATCTACCAACCGCAAGCTACTGTGTCACC 285
    |||||
Db 398 ACGATTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 339
    |||||
OY 286 ACCAAGACGTAACCAAGACACTACCAAGCAACTACCAAGACTAGCACTAGCCGCT 345
    |||||
Db 338 ACTCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 279
    |||||
OY 346 GCTTCTACTTCACCTCTTCTTCTGCTGTTACAAGTCATCTGCGGTAATCTGGC 405
    |||||
Db 278 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 219
    |||||
OY 406 AGTGTTCACACTCGTTATGGATTGTGTAAGCTCTTGCAGCTGGCTGGAAGA 465
    |||||
Db 218 ATTCTACTACMCTACTGSSCTTCTTCTCTACTATTCTAAMAACCTGTACTACMGA 159
    |||||
OY 466 GCTTCTGCTACTGCTCT 483
    |||||
Db 158 AACCTGTCTACTGCTACT 141
    |||||
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Job time : 1373.68 secs

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